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1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/668,314A

DATE: 05/24/2001

TIME: 17:58:43

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4 <110> APPLICANT: Gurney, Mark
5 Bienkowski, Michael J.
7 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
USES

8 THEREOF

10 <130> FILE REFERENCE: 28341/6280NCP
12 <140> CURRENT APPLICATION NUMBER: 09/668,314A
13 <141> CURRENT FILING DATE: 2000-09-22
15 <150> PRIOR APPLICATION NUMBER: 60/169,232
16 <151> PRIOR FILING DATE: 1999-12-06
18 <150> PRIOR APPLICATION NUMBER: 09/416,901
19 <151> PRIOR FILING DATE: 1999-10-13
21 <150> PRIOR APPLICATION NUMBER: 60/155,493
22 <151> PRIOR FILING DATE: 1999-09-23
24 <150> PRIOR APPLICATION NUMBER: 09/404,133
25 <151> PRIOR FILING DATE: 1999-09-23
27 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881
28 <151> PRIOR FILING DATE: 1999-09-23
30 <150> PRIOR APPLICATION NUMBER: 60/101,594
31 <151> PRIOR FILING DATE: 1998-09-24
33 <160> NUMBER OF SEQ ID NOS: 82
35 <170> SOFTWARE: PatentIn Ver. 2.0
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 1804
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
42 <400> SEQUENCE: 1

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45 cgcgtagttg cgcccccccc gggacccggg acccctgccc agcgccaacgc cgacggcttg 180
46 gcgctcgccc tggagcctgc cctggcgctcc cccgcgggcg ccgccaactt cttggccatg 240
47 gtagacaacc tgcaggggga ctctggccgc ggctactacc tggagatgct gatcgggacc 300
48 cccccgcaga agctacagat tctcgttgac actggaagca gtaactttgc cgtggcagga 360
49 accccgcact cctacataga cacgtacttt gacacagaga ggtctagcac ataccgctcc 420
50 aagggccttg acgtcacagt gaagtacaca caagggaagct ggacgggctt cgttggggaa 480
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55 ggatctggga ccaacggagg tagtcttgct ttgggtggaa ttgaaccaag tttgtataaa 780
56 ggagacatct ggtatacccc tattaaggaa gagtgttact accagataga aattctgaaa 840
57 ttggaaatg gaggcaaaag ccttaatctg gactgcagag agtataacgc agacaaggcc 900
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60 cagctggcgt gctggacgaa ttcggaaaca ccttggtctt acttccctaa aatctccatc 1080
61 tacctgagag atgagaactc cagcaggta ttccgtatca caatcctgcc tcagctttac 1140
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66 cagtctttga gcgagcccat ttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440
67 gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccggtgtca gcgtcgcccc 1500
68 cgtgaccctg aggtcgtcaa tgatgagtc tctctgggtca gacatcgctg gaaatgaata 1560
69 gccaggcctg acctcaagca accatgaact cagctattaa gaaaatcaca tttccagggc 1620
70 agcagccggg atcgatgggt gcgctttctc ctgtgccac ccgtcttcaa tctctgttct 1680
71 gctcccagat gccttctaga ttcaactgtc ttgtattctt gatittcaag ctttcaaatc 1740
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76 <211> LENGTH: 518
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapiens
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82 1 5 10 15
84 Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
85 20 25 30
87 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
88 35 40 45
90 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
91 50 55 60
93 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
94 65 70 75 80
96 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
97 85 90 95
99 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100 100 105 110
102 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
103 115 120 125
105 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
106 130 135 140
108 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
109 145 150 155 160
111 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
112 165 170 175
115 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
116 180 185 190
118 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
119 195 200 205
121 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
122 210 215 220
124 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
125 225 230 235 240
128 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
129 245 250 255
131 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
132 260 265 270

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140 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
141 305          310          315          320
143 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
144          325          330          335
146 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
147          340          345          350
149 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
150          355          360          365
152 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
153          370          375          380
155 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
156 385          390          395          400
158 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
159          405          410          415
161 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
162          420          425          430
164 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
165          435          440          445
167 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
168          450          455          460
171 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
172 465          470          475          480
174 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
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180 Val Arg His Arg Trp Lys
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184 <210> SEQ ID NO: 3

185 <211> LENGTH: 2070

186 <212> TYPE: DNA

187 <213> ORGANISM: Homo sapiens

189 <400> SEQUENCE: 3

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192 ctgcggtgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
193 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
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200 ctggtaaaag agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
201 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc 720

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204 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
205 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
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207 ttcccagtc tctcactcta cctaattggg gaggttacca accagtcctt ccgcatcacc 1080
208 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
209 tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1200
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215 aagtgaggag gcccatgggc agaagataga gattcccctg gaccacacct ccgtggttca 1560
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218 ggactgtacc tgtaggaaac agaaaagaga agaaaagaagc actctgctgg cggaataact 1740
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226 <210> SEQ ID NO: 4

227 <211> LENGTH: 501

228 <212> TYPE: PRT

229 <213> ORGANISM: Homo sapiens

231 <400> SEQUENCE: 4

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236           20           25           30
238 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
239           35           40           45
241 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
242           50           55           60
244 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
245           65           70           75           80
247 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
248           85           90           95
250 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
251           100          105          110
254 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
255           115          120          125
257 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
258           130          135          140
260 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
261           145          150          155          160
263 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp

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270          195          200          205
272 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
273          210          215          220
275 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
276 225          230          235          240
278 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
279          245          250          255
282 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
283          260          265          270
285 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
286          275          280          285
288 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
289          290          295          300
291 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
292 305          310          315          320
294 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
295          325          330          335
297 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
298          340          345          350
300 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
301          355          360          365
303 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
304          370          375          380
306 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
307 385          390          395          400
309 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
310          405          410          415
312 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
313          420          425          430
315 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
316          435          440          445
318 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
319          450          455          460
321 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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VERIFICATION SUMMARY

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